

Rec'd PCT/P:

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/523,047  
Source: PCF  
Date Processed by STIC: 3/3/06

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 03/03/2006

PATENT APPLICATION: US/10/523,047

TIME: 12:59:41

Input Set : A:\SEQLIST.TXT

Output Set: N:\CRF4\03032006\J523047.raw

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4 <110> APPLICANT: LANE, Roger Michael
5 POLYMERPOULOS, Mihael Hristos
7 <120> TITLE OF INVENTION: METHODS FOR THE TREATMENT OF DEMENTIA
8 BASED ON APO E GENOTYPE
11 <130> FILE REFERENCE: DV/4-32609A/USN
13 <140> CURRENT APPLICATION NUMBER: 10/523,047
C--> 14 <141> CURRENT FILING DATE: 2005-02-02
16 <150> PRIOR APPLICATION NUMBER: PCT/EP03/008719
17 <151> PRIOR FILING DATE: 2003-07-06
19 <150> PRIOR APPLICATION NUMBER: 60/401,694
20 <151> PRIOR FILING DATE: 2002-07-07
22 <160> NUMBER OF SEQ ID NOS: 6
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1223
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
32 <221> NAME/KEY: mRNA
33 <222> LOCATION: (1)...(1223)
34 <223> OTHER INFORMATION: ApoE mRNA, e2 variant
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (84)...(1037)
W--> 39 <221> sig_peptide
40 <222> LOCATION: (84)...(137)
W--> 42 <221> mat_peptide
43 <222> LOCATION: (138)...(1037)
W--> 45 <400> 1
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47 actggccaat cacaggcagg aag atg aag gtt ctg tgg gct gcg ttg ctg gtc 113
48 Met Lys Val Leu Trp Ala Ala Leu Leu Val
49 -15 -10
51 aca ttc ctg gca gga tgc cag gcc aag gtg gag caa gcg gtg gag aca 161
52 Thr Phe Leu Ala Gly Cys Gln Ala Lys Val Glu Gln Ala Val Glu Thr
53 -5 1 5
55 gag ccg gag ccc gag ctg cgc cag cag acc gag tgg cag agc ggc cag 209
56 Glu Pro Glu Pro Glu Leu Arg Gln Gln Thr Glu Trp Gln Ser Gly Gln
57 10 15 20
59 cgc tgg gaa ctg gca ctg ggt cgc ttt tgg gat tac ctg cgc tgg gtg 257
60 Arg Trp Glu Leu Ala Leu Gly Arg Phe Trp Asp Tyr Leu Arg Trp Val
61 25 30 35 40
63 cag aca ctg tct gag cag gtg cag gag gag ctg ctc agc tcc cag gtc 305
64 Gln Thr Leu Ser Glu Gln Val Gln Glu Glu Leu Leu Ser Ser Gln Val

```

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65          45          50          55
67 acc cag gaa ctg agg gcg ctg atg gac gag acc atg aag gag ttg aag 353
68 Thr Gln Glu Leu Arg Ala Leu Met Asp Glu Thr Met Lys Glu Leu Lys
69          60          65          70
71 gcc tac aaa tcg gaa ctg gag gaa caa ctg acc ccg gtg gcg gag gag 401
72 Ala Tyr Lys Ser Glu Leu Glu Glu Gln Leu Thr Pro Val Ala Glu Glu
73          75          80          85
75 acg cgg gca cgg ctg tcc aag gag ctg cag gcg gcg cag gcc cgg ctg 449
76 Thr Arg Ala Arg Leu Ser Lys Glu Leu Gln Ala Ala Gln Ala Arg Leu
77          90          95          100
79 ggc gcg gac atg gag gac gtg tgc ggc cgc ctg gtg cag tac cgc ggc 497
80 Gly Ala Asp Met Glu Asp Val Cys Gly Arg Leu Val Gln Tyr Arg Gly
81 105          110          115          120
83 gag gtg cag gcc atg ctc ggc cag agc acc gag gag ctg cgg gtg cgc 545
84 Glu Val Gln Ala Met Leu Gly Gln Ser Thr Glu Glu Leu Arg Val Arg
85          125          130          135
87 ctc gcc tcc cac ctg cgc aag ctg cgt aag cgg ctc ctc cgc gat gcc 593
88 Leu Ala Ser His Leu Arg Lys Leu Arg Lys Arg Leu Leu Arg Asp Ala
89          140          145          150
91 gat gac ctg cag aag tgc ctg gca gtg tac cag gcc ggg gcc cgc gag 641
92 Asp Asp Leu Gln Lys Cys Leu Ala Val Tyr Gln Ala Gly Ala Arg Glu
93          155          160          165
95 ggc gcc gag cgc ggc ctc agc gcc atc cgc gag cgc ctg ggg ccc ctg 689
96 Gly Ala Glu Arg Gly Leu Ser Ala Ile Arg Glu Arg Leu Gly Pro Leu
97          170          175          180
99 gtg gaa cag ggc cgc gtg cgg gcc gcc act gtg ggc tcc ctg gcc ggc 737
100 Val Glu Gln Gly Arg Val Arg Ala Ala Thr Val Gly Ser Leu Ala Gly
101 185          190          195          200
103 cag ccg cta cag gag cgg gcc cag gcc tgg ggc gag cgg ctg cgc gcg 785
104 Gln Pro Leu Gln Glu Arg Ala Gln Ala Trp Gly Glu Arg Leu Arg Ala
105          205          210          215
107 cgg atg gag gag atg ggc agc cgg acc cgc gac cgc ctg gac gag gtg 833
108 Arg Met Glu Glu Met Gly Ser Arg Thr Arg Asp Arg Leu Asp Glu Val
109          220          225          230
111 aag gag cag gtg gcg gag gtg cgc gcc aag ctg gag gag cag gcc cag 881
112 Lys Glu Gln Val Ala Glu Val Arg Ala Lys Leu Glu Glu Gln Ala Gln
113          235          240          245
115 cag ata cgc ctg cag gcc gag gcc ttc cag gcc cgc ctc aag agc tgg 929
116 Gln Ile Arg Leu Gln Ala Glu Ala Phe Gln Ala Arg Leu Lys Ser Trp
117          250          255          260
119 ttc gag ccc ctg gtg gaa gac atg cag cgc cag tgg gcc ggg ctg gtg 977
120 Phe Glu Pro Leu Val Glu Asp Met Gln Arg Gln Trp Ala Gly Leu Val
121 265          270          275          280
123 gag aag gtg cag gct gcc gtg ggc acc agc gcc gcc cct gtg ccc agc 1025
124 Glu Lys Val Gln Ala Ala Val Gly Thr Ser Ala Ala Pro Val Pro Ser
125          285          290          295
127 gac aat cac tga acgccgaagc ctgcagccat gcgacccac gccaccccg 1077
128 Asp Asn His *
131 gcctctgcc tccgcgcagc ctgcagcggg agaccctgtc cccgccccag ccgtcctcct 1137

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132 ggggtggacc ctagttaa aaagattcac caagtttcac gcaaaaaaaaa aaaaaaaaaa 1197
133 aaaaaaaaaa aaaaaaaaaa aaaaaa 1223
135 <210> SEQ ID NO: 2
136 <211> LENGTH: 317
137 <212> TYPE: PRT
138 <213> ORGANISM: Homo sapiens
140 <220> FEATURE:
141 <221> NAME/KEY: SIGNAL
142 <222> LOCATION: (1)...(18)
144 <400> SEQUENCE: 2
145 Met Lys Val Leu Trp Ala Ala Leu Leu Val Thr Phe Leu Ala Gly Cys
146 -15 -10 -5
147 Gln Ala Lys Val Glu Gln Ala Val Glu Thr Glu Pro Glu Pro Glu Leu
148 1 5 10
149 Arg Gln Gln Thr Glu Trp Gln Ser Gly Gln Arg Trp Glu Leu Ala Leu
150 15 20 25 30
151 Gly Arg Phe Trp Asp Tyr Leu Arg Trp Val Gln Thr Leu Ser Glu Gln
152 35 40 45
153 Val Gln Glu Glu Leu Leu Ser Ser Gln Val Thr Gln Glu Leu Arg Ala
154 50 55 60
155 Leu Met Asp Glu Thr Met Lys Glu Leu Lys Ala Tyr Lys Ser Glu Leu
156 65 70 75
157 Glu Glu Gln Leu Thr Pro Val Ala Glu Glu Thr Arg Ala Arg Leu Ser
158 80 85 90
159 Lys Glu Leu Gln Ala Ala Gln Ala Arg Leu Gly Ala Asp Met Glu Asp
160 95 100 105 110
161 Val Cys Gly Arg Leu Val Gln Tyr Arg Gly Glu Val Gln Ala Met Leu
162 115 120 125
163 Gly Gln Ser Thr Glu Glu Leu Arg Val Arg Leu Ala Ser His Leu Arg
164 130 135 140
165 Lys Leu Arg Lys Arg Leu Leu Arg Asp Ala Asp Asp Leu Gln Lys Cys
166 145 150 155
167 Leu Ala Val Tyr Gln Ala Gly Ala Arg Glu Gly Ala Glu Arg Gly Leu
168 160 165 170
169 Ser Ala Ile Arg Glu Arg Leu Gly Pro Leu Val Glu Gln Gly Arg Val
170 175 180 185 190
171 Arg Ala Ala Thr Val Gly Ser Leu Ala Gly Gln Pro Leu Gln Glu Arg
172 195 200 205
173 Ala Gln Ala Trp Gly Glu Arg Leu Arg Ala Arg Met Glu Glu Met Gly
174 210 215 220
175 Ser Arg Thr Arg Asp Arg Leu Asp Glu Val Lys Glu Gln Val Ala Glu
176 225 230 235
177 Val Arg Ala Lys Leu Glu Glu Gln Ala Gln Gln Ile Arg Leu Gln Ala
178 240 245 250
179 Glu Ala Phe Gln Ala Arg Leu Lys Ser Trp Phe Glu Pro Leu Val Glu
180 255 260 265 270
181 Asp Met Gln Arg Gln Trp Ala Gly Leu Val Glu Lys Val Gln Ala Ala
182 275 280 285
183 Val Gly Thr Ser Ala Ala Pro Val Pro Ser Asp Asn His

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Input Set : A:\SEQLIST.TXT

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184                290                295
187 <210> SEQ ID NO: 3
188 <211> LENGTH: 1223
189 <212> TYPE: DNA
190 <213> ORGANISM: Homo sapiens
192 <220> FEATURE:
193 <221> NAME/KEY: mRNA
194 <222> LOCATION: (1)...(1223)
195 <223> OTHER INFORMATION: ApoE mRNA, e3 variant
197 <221> NAME/KEY: CDS
198 <222> LOCATION: (84)...(1037)
W--> 200 <221> sig_peptide
      201 <222> LOCATION: (84)...(137)
W--> 203 <221> mat_peptide
      204 <222> LOCATION: (138)...(1037)
W--> 206 <400> 3
207 gggatccttg agtcctactc agccccagcg gaggtgaagg acgtccttcc ccaggagccg 60
208 actggccaat cacaggcagg aag atg aag gtt ctg tgg gct gcg ttg ctg gtc 113
209          Met Lys Val Leu Trp Ala Ala Leu Leu Val
210          -15          -10
212 aca ttc ctg gca gga tgc cag gcc aag gtg gag caa gcg gtg gag aca 161
213 Thr Phe Leu Ala Gly Cys Gln Ala Lys Val Glu Gln Ala Val Glu Thr
214          -5          1          5
216 gag ccg gag ccc gag ctg cgc cag cag acc gag tgg cag agc ggc cag 209
217 Glu Pro Glu Pro Glu Leu Arg Gln Gln Thr Glu Trp Gln Ser Gly Gln
218          10          15          20
220 cgc tgg gaa ctg gca ctg ggt cgc ttt tgg gat tac ctg cgc tgg gtg 257
221 Arg Trp Glu Leu Ala Leu Gly Arg Phe Trp Asp Tyr Leu Arg Trp Val
222          25          30          35          40
224 cag aca ctg tct gag cag gtg cag gag gag ctg ctc agc tcc cag gtc 305
225 Gln Thr Leu Ser Glu Gln Val Gln Glu Glu Leu Leu Ser Ser Gln Val
226          45          50          55
228 acc cag gaa ctg agg gcg ctg atg gac gag acc atg aag gag ttg aag 353
229 Thr Gln Glu Leu Arg Ala Leu Met Asp Glu Thr Met Lys Glu Leu Lys
230          60          65          70
232 gcc tac aaa tcg gaa ctg gag gaa caa ctg acc ccg gtg gcg gag gag 401
233 Ala Tyr Lys Ser Glu Leu Glu Glu Gln Leu Thr Pro Val Ala Glu Glu
234          75          80          85
236 acg cgg gca cgg ctg tcc aag gag ctg cag gcg gcg cag gcc cgg ctg 449
237 Thr Arg Ala Arg Leu Ser Lys Glu Leu Gln Ala Ala Gln Ala Arg Leu
238          90          95          100
240 ggc gcg gac atg gag gac gtg tgc ggc cgc ctg gtg cag tac cgc ggc 497
241 Gly Ala Asp Met Glu Asp Val Cys Gly Arg Leu Val Gln Tyr Arg Gly
242          105          110          115          120
244 gag gtg cag gcc atg ctc ggc cag agc acc gag gag ctg cgg gtg cgc 545
245 Glu Val Gln Ala Met Leu Gly Gln Ser Thr Glu Glu Leu Arg Val Arg
246          125          130          135
248 ctc gcc tcc cac ctg cgc aag ctg cgt aag cgg ctc ctc cgc gat gcc 593
249 Leu Ala Ser His Leu Arg Lys Leu Arg Lys Arg Leu Leu Arg Asp Ala

```

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250          140          145          150
252 gat gac ctg cag aag cgc ctg gca gtg tac cag gcc ggg gcc cgc gag 641
253 Asp Asp Leu Gln Lys Arg Leu Ala Val Tyr Gln Ala Gly Ala Arg Glu
254          155          160          165
256 ggc gcc gag cgc ggc ctc agc gcc atc cgc gag cgc ctg ggg ccc ctg 689
257 Gly Ala Glu Arg Gly Leu Ser Ala Ile Arg Glu Arg Leu Gly Pro Leu
258          170          175          180
260 gtg gaa cag ggc cgc gtg cgg gcc gcc act gtg ggc tcc ctg gcc ggc 737
261 Val Glu Gln Gly Arg Val Arg Ala Ala Thr Val Gly Ser Leu Ala Gly
262 185          190          195          200
264 cag ccg cta cag gag cgg gcc cag gcc tgg ggc gag cgg ctg cgc gcg 785
265 Gln Pro Leu Gln Glu Arg Ala Gln Ala Trp Gly Glu Arg Leu Arg Ala
266          205          210          215
268 cgg atg gag gag atg ggc agc cgg acc cgc gac cgc ctg gac gag gtg 833
269 Arg Met Glu Glu Met Gly Ser Arg Thr Arg Asp Arg Leu Asp Glu Val
270          220          225          230
272 aag gag cag gtg gcg gag gtg cgc gcc aag ctg gag gag cag gcc cag 881
273 Lys Glu Gln Val Ala Glu Val Arg Ala Lys Leu Glu Glu Gln Ala Gln
274          235          240          245
276 cag ata cgc ctg cag gcc gag gcc ttc cag gcc cgc ctc aag agc tgg 929
277 Gln Ile Arg Leu Gln Ala Glu Ala Phe Gln Ala Arg Leu Lys Ser Trp
278          250          255          260
280 ttc gag ccc ctg gtg gaa gac atg cag cgc cag tgg gcc ggg ctg gtg 977
281 Phe Glu Pro Leu Val Glu Asp Met Gln Arg Gln Trp Ala Gly Leu Val
282 265          270          275          280
284 gag aag gtg cag gct gcc gtg ggc acc agc gcc gcc cct gtg ccc agc 1025
285 Glu Lys Val Gln Ala Ala Val Gly Thr Ser Ala Ala Pro Val Pro Ser
286          285          290          295
288 gac aat cac tga acgccgaagc ctgcagccat gcgaccccccac gccaccccg 1077
289 Asp Asn His *
292 gcctcctgcc tccgcgcagc ctgcagcggg agaccctgtc cccgccccag ccgtcctcct 1137
293 ggggtggacc ctagtttaaat aaagattcac caagttttcac gcaaaaaaaaa aaaaaaaaaa 1197
294 aaaaaaaaaa aaaaaaaaaa aaaaaa 1223
296 <210> SEQ ID NO: 4
297 <211> LENGTH: 317
298 <212> TYPE: PRT
299 <213> ORGANISM: Homo sapiens
301 <220> FEATURE:
302 <221> NAME/KEY: SIGNAL
303 <222> LOCATION: (1)...(18)
305 <400> SEQUENCE: 4
306 Met Lys Val Leu Trp Ala Ala Leu Leu Val Thr Phe Leu Ala Gly Cys
307          -15          -10          -5
308 Gln Ala Lys Val Glu Gln Ala Val Glu Thr Glu Pro Glu Pro Glu Leu
309          1          5          10
310 Arg Gln Gln Thr Glu Trp Gln Ser Gly Gln Arg Trp Glu Leu Ala Leu
311 15          20          25          30
312 Gly Arg Phe Trp Asp Tyr Leu Arg Trp Val Gln Thr Leu Ser Glu Gln
313          35          40          45

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## VERIFICATION SUMMARY

DATE: 03/03/2006

PATENT APPLICATION: US/10/523,047

TIME: 12:59:42

Input Set : A:\SEQLIST.TXT

Output Set: N:\CRF4\03032006\J523047.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:39 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:42 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:45 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:200 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:203 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:206 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:361 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5  
L:364 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5  
L:367 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5